

ABSTRACT

The present invention relates generally to a method for identifying or otherwise detecting a nucleotide repeat region having a particular length in a nucleic acid molecule. Varying lengths of the repeat region at particular genetic locations represent nucleotide length polymorphisms. The present invention provides, therefore, a method for identifying a nucleotide length polymorphism such as associated with a particular human individual or animal or mammalian subject or for a disease condition or a predisposition for a disease condition to develop in a particular individual or subject. The method of the present invention is also useful for identifying and/or typing micro-organisms including yeasts and lower uni- and multi-cellular organisms as well as prokaryotic micro-organisms. The method of the present invention is further useful in genotyping subjects including humans. The method of the present invention is referred to herein as a "ligase-assisted spacer addition" assay or "LASA" assay.